



SEQUENCE LISTING

<110> GALZI, JEAN-LUC
ALIX, PHILIPPE

<120> USE OF A FLUORESCENT PROTEIN FOR DETECTING INTERACTION
BETWEEN A TARGET PROTEIN AND ITS LIGAND

<130>

<140>
<141>

<150> PCT/FR98/01136
<151> 1998-06-04

<150> FR 97/06977
<151> 1997-06-05

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 798

<212> DNA

<213> Aequorea Victoria

<220>

<221> CDS

<222> (1)...(795)

<400> 1

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc aac cac atg aag 240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag		336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100	105	110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac		432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac		480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
145	150	155
160		
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc		528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		
165	170	175
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc		576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
180	185	190
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg		624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
195	200	205
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc		672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
210	215	220
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tac		720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Tyr		
225	230	235
240		
tca gat ctc gag ctc aag ctt cga att ctg cag tcg acg gta ccg cg		768
Ser Asp Leu Glu Leu Lys Leu Arg Ile Leu Gln Ser Thr Val Pro Arg		
245	250	255
gcc cg gat cca ccg gat cta gat aac tga		798
Ala Arg Asp Pro Pro Asp Leu Asp Asn		
260	265	
<210> 2		
<211> 265		
<212> PRT		
<213> Aequorea victoria		
<400> 2		
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
1	5	10
15		
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20	25	30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Tyr
 225 230 235 240

 Ser Asp Leu Glu Leu Lys Leu Arg Ile Leu Gln Ser Thr Val Pro Arg
 245 250 255

 Ala Arg Asp Pro Pro Asp Leu Asp Asn
 260 265

<210> 3
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: spacer sequence

<400> 3
 Gly Gly Gly Gly Ser
 1 5

<210> 4
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cyclopeptide

<400> 4
Gln Trp Phe Gly Leu Met
1 5

<210> 5
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 5
ggtcgcacc ctgtacaaga agggcgagg 29

<210> 6
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 6
cacgagagga tgtacaacct cgagcgcaca gtcacc 36

<210> 7
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 7
gtacccagac accagctagc agatctgaag cttcgccatc aggc 44

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
ggagagttcc aactcgagaa aagaaaagaag ggcgaggag 39

<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
gtcagctgtt tctgcggcgc gctaaggctg ggccctt 36

<210> 10
<211> 51
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 10
ttagttctaa actagcggcc gcactagtcc tccatgaaca cttcagcccc a 51

<210> 11
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
cttgaaccta tagctagcct cgagtcagca ttggcgggag gg 42

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
cctgctgtct cagatctcat caccgtcc 28

<210> 13
<211> 47

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 13
cagatcatta gttgtacagg aaagatcttg aggatcctgg agtgaag 47

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 14
ggcccaagct tatgtcagga tccggggat 29

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 15
cgccccgctcg agtcacaagg ccacagat 30

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 16
gttgacaagg ttccggatcc a 21

<210> 17
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 17
agcacagagg gcagtagcaa tgaggatgac agcgaggcgt gccgcggaga ctttcattgg 60
atcccaagc ttatcaac 78

<210> 18
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 18
attgctactg ccctctgtgc tcctgcatact gcctcccat attcctcgga caccacacca 60
tgctgcttgc cctacatt 78

<210> 19
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 19
gcacttgcctt ctgggttaga aatactcattt gatgtggca caaggcagtgc ggcgggcaat 60
gtaggcgaag cagcatgg 78

<210> 20
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 20
gcacttgcctt ctgggttaga aatactcattt gatgtggca cggggcagtgc ggcgagcaat 60
gtaggcaaaag cagcatgg 78

<210> 21
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 21

ctagctcata tccagcgagt tgatgtactc ccgaaccat ttcttctctg ggttggcaca	60
aacttgacg	69
<210> 22	
<211> 50	
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<400> 22	
aactcgctgg agatgagcta ggccggccgct cgaggctcgac ctagtcacta	50
<210> 23	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
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<223> Description of Artificial Sequence:	
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<400> 23	
tagtgactag gtcgacacctcg a	21
<210> 24	
<211> 41	
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<400> 24	
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<210> 25	
<211> 43	
<212> DNA	
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Oligonucleotide	
<400> 25	
ccgctcgagt taatctagaa ggaccaaatt gtactccttc aag	43